

SEQUENCE LISTING

<110> Universitaet Zuerich

<120> In vivo model system for type-2 diabetes

<130> Universitaet Zuerich

<140>

<141>

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 2907

<212> DNA

<213> *Drosophila melanogaster*

<400> 1

atggcatcaa tatcggatga cggcatggcg ctgagtggt acctcaagaa gctgaagacc 60

atgaagaaga agttctttgt gctgtacgag gagacgagca cttcggcagc ccggctggag 120

tactacgata ccgaaaagaa gttcctgcaa agagccgagc caaaaagggt tatatatctg 180

aagaattgct tcaacatcaa tcggcggttgc gacaccaagc atagatttgt catttgctc 240

tcctccagag acgggtggatt cggcatcggtt ctcgagaacg aaaatgattt acgcaaatgg 300

ttggacaaac tactagttct acaaaggaac atagccaatt cgaatggaac agcgcactca 360

ccttatgacc acgtttggca agttgtcatt caaaaagaagg gtatttcgga gaaagttgga 420

atcaccggaa cctaccactg ttgccttact tcaaaatccc tgacattcggtt gtgcattgg 480

ccggagaaga cgcccaatgg cgaggatcgc gttgcgagca ttgaaatact tttgaccacg 540

atcaggcgat gcggtcatgc atccccacaa tgtatattct acgtggaact tggccggccaa 600

agtgtcttgg gatctgggtga tctgtggatg gagacggata acgcagctat tgctactaat 660

atgcacaaaca cgatactgag cgctatgtca gccaacacag agtcgaacac gaatttaata 720

aacgtttatc agaatagacc tgacttaagt cacgagccca tgagaaagcg atcgtcgct 780

gcaaacgaag catcgaagcc gataaacgta aatgtcatac aaaatagtca aaactctctc 840

gaattgcgca gctgcagtgc gccccataac tatggttcg gcagagagag atgcgatagc 900
ttaccaacca gaaatggaac cctaagcgag tccagcaatc aaacgtactt tggttccaac 960
catggactgc gatccaatac tatatctggc atccgtccgc actcaaccaa caagcatagt 1020
aatagtccaa cgttcaccat gccattaaga tgctcagaat ccgaagagtc atcaattagt 1080
gtcgatgaat ccgacgacaa cggcagttt agccactaca gattaaacac gcggtcatct 1140
gagacggcaa ttcctgagga aaacattgat gactttgcca gtgcggaatt atttagcaaa 1200
gtcaccgaac aaaatgtaaag tgacgaaaac tacataccga tgaatccagt caatcctacc 1260
gatgctatcc atgaaaagga gaaggctgat atgcagagat tggaagatgc ttcgctgcat 1320
ttcaacttgc cgagcacgc gtcggaaaag ctgctaagg attttgatct ggactctgat 1380
aaccaatgct gtcgtcccat tcgcccstat tcgataggca acaaggttga gcatttaaag 1440
tttaataagc gcctgggaca cttgaatgat acgggacaga atccgaatcg cgtgcgagcc 1500
tactcggttg gtcggaaatc gaagataccg cgctgcgacc tgcagcgagt gtcctcggt 1560
gaggacaata aacatgagtt cacagcgaat aggagtcaga gtagcattac caaggaagga 1620
accagctatg gcagcagtgc caatcgacaa aagaagtcca caagtgcctcc actcctcagt 1680
ctgaagaacc agataaactc cgaccgaatg agtgacttaa tggaaattga ttttcaccaa 1740
gcaaccaatt tggaaaagca gaagttcatc aagaataatg aaattccgaa atacattgaa 1800
aacgtgttcc caaaagcccc gcgaacggat agctccagcc taactctgca cgccacaagt 1860
caaaaggaca tttcaatgg caccaaacta aataacactg cgatcacatc cgaggatggt 1920
tacctcgaga tgaagccagt cggtaatgga tacactccca gttcgaatttgc cctgccaatg 1980
aaagtggaga aactcaagct atccgactat cagacagcac cgccactcac cgcaacagcc 2040
gcaccagtgc acgatttaaa caaaatttgc acatacaata tatccgctga gaaatggaga 2100
gaacagccca gcagaagcga ggaaaagaag tcgaactcgc cattgaatga caacacctt 2160
agctcgaaac ccacaaatgt cgagagtaca agcaaaagcc atgatgttca ttcagcaat 2220
caaattgatt gcgagaaaagt gtgcgcgcag agcagcgata agctaaataa tcatctggcc 2280

gacaagattg tcgagaacaa caatttggat ataggcgggc atgaggaaaa gaagttggtt 2340
cattcgataa gcagcgaaga ctacacacaa atcaaggaca aatcgaatga tttcacaaaa 2400
tttaacgaag ccggctacaa aattctgcaa attaaaagcg acagctcact catctcatcg 2460
aagctataacc aaaagggtat acacaaggat aacttggagc gttcgcagag acttacagag 2520
agtgtgaata cgattcccga taatgccacc gccaccgcgg tgagcagcag ctcactcacc 2580
aaattcaata taaattcagc aaagccagcc gccgcccgg attcgcgtag cactggcaca 2640
gatccaagta caccacagaa cattctacag attaaagatt tgaatttccc ctcaaggctcg 2700
tcgtctcgca tatcccagcc ggagctgcac tacgccagcc tagatttcc ccattgcagt 2760
ggccaaaatc cagctaaata cctgaagaga ggatcacgcg aatcggcgcc ggtgtccgca 2820
tgcccgagg atggaatac ctatgcgaaa atcgactttg accaatccga ctccctttcc 2880
tcctcatcga acatatttaa tacgtaa 2907

<210> 2

<211> 2907

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(2907)

<400> 2

atg gca tca ata tcg gat gac ggc atg gcg ctg agt ggc tac ctc aag 48

Met Ala Ser Ile Ser Asp Asp Gly Met Ala Leu Ser Gly Tyr Leu Lys

1

5

10

15

aag ctg aag acc atg aag aag ttc ttt gtg ctg tac gag gag acg 96

Lys Leu Lys Thr Met Lys Lys Phe Phe Val Leu Tyr Glu Glu Thr

20

25

30

agc act tcg gca gcc cgg ctg gag tac tac gat acc gaa aag aag ttc 144

Ser Thr Ser Ala Ala Arg Leu Glu Tyr Tyr Asp Thr Glu Lys Phe

35

40

45

ctg caa aga gcc gag cca aaa agg gtt ata tat ctg aag aat tgc ttc 192

Leu Gln Arg Ala Glu Pro Lys Arg Val Ile Tyr Leu Lys Asn Cys Phe

50	55	60	
aac atc aat cgc cgt ttg gac acc aag cat aga ttt gtc att gtg ctc 240			
Asn Ile Asn Arg Arg Leu Asp Thr Lys His Arg Phe Val Ile Val Leu			
65	70	75	80
tcc tcc aga gac ggt gga ttc ggc atc gtt ctc gag aac gaa aat gat 288			
Ser Ser Arg Asp Gly Gly Phe Gly Ile Val Leu Glu Asn Glu Asn Asp			
85	90	95	
tta cgc aaa tgg ttg gac aaa cta cta gtt cta caa agg aac ata gcc 336			
Leu Arg Lys Trp Leu Asp Lys Leu Leu Val Leu Gln Arg Asn Ile Ala			
100	105	110	
aat tcg aat gga aca gcg cac tca cct tat gac cac gtt tgg caa gtt 384			
Asn Ser Asn Gly Thr Ala His Ser Pro Tyr Asp His Val Trp Gln Val			
115	120	125	
gtc att caa aag aag ggt att tcg gag aaa gtt gga atc acc gga acc 432			
Val Ile Gln Lys Lys Gly Ile Ser Glu Lys Val Gly Ile Thr Gly Thr			
130	135	140	
tac cac tgt tgc ctt act tca aaa tcc ctg aca ttc gtg tgc att gga 480			
Tyr His Cys Cys Leu Thr Ser Lys Ser Leu Thr Phe Val Cys Ile Gly			
145	150	155	160
ccg gag aag acg ccc aat ggc gag gat cgc gtt gcg agc att gaa ata 528			
Pro Glu Lys Thr Pro Asn Gly Glu Asp Arg Val Ala Ser Ile Glu Ile			
165	170	175	
ctt ttg acc acg atc agg cga tgc ggt cat gca tcc cca caa tgt ata 576			
Leu Leu Thr Thr Ile Arg Arg Cys Gly His Ala Ser Pro Gln Cys Ile			
180	185	190	
ttc tac gtg gaa ctt ggc cgc caa agt gtc ttg gga tct ggt gat ctg 624			
Phe Tyr Val Glu Leu Gly Arg Gln Ser Val Leu Gly Ser Gly Asp Leu			
195	200	205	
tgg atg gag acg gat aac gca gct att gct act aat atg cac aac acg 672			
Trp Met Glu Thr Asp Asn Ala Ala Ile Ala Thr Asn Met His Asn Thr			
210	215	220	
ata ctg agc gct atg tca gcc aaa aca gag tcg aac acg aat tta ata 720			
Ile Leu Ser Ala Met Ser Ala Lys Thr Glu Ser Asn Thr Asn Leu Ile			
225	230	235	240
aac gtt tat cag aat aga cct gac tta agt cac gag ccc atg aga aag 768			
Asn Val Tyr Gln Asn Arg Pro Asp Leu Ser His Glu Pro Met Arg Lys			

245	250	255	
			816
cga tcg tcg tct gca aac gaa gca tcg aag ccg ata aac gta aat gtc Arg Ser Ser Ser Ala Asn Glu Ala Ser Lys Pro Ile Asn Val Asn Val			816
260	265	270	
			864
ata caa aat agt caa aac tct ctc gaa ttg cgc agc tgc agt tcg ccc Ile Gln Asn Ser Gln Asn Ser Leu Glu Leu Arg Ser Cys Ser Ser Pro			864
275	280	285	
			912
cat aac tat ggt ttc ggc aga gag aga tgc gat agc tta cca acc aga His Asn Tyr Gly Phe Gly Arg Glu Arg Cys Asp Ser Leu Pro Thr Arg			912
290	295	300	
			960
aat gga acc cta agc gag tcc agc aat caa acg tac ttt ggt tcc aac Asn Gly Thr Leu Ser Glu Ser Ser Asn Gln Thr Tyr Phe Gly Ser Asn			960
305	310	315	320
			1008
cat gga ctg cga tcc aat act ata tct ggc atc cgt ccg cac tca acc His Gly Leu Arg Ser Asn Thr Ile Ser Gly Ile Arg Pro His Ser Thr			1008
325	330	335	
			1056
aac aag cat agt aat agt cca acg ttc acc atg cca tta aga tgc tca Asn Lys His Ser Asn Ser Pro Thr Phe Thr Met Pro Leu Arg Cys Ser			1056
340	345	350	
			1104
gaa tcc gaa gag tca tca att agt gtc gat gaa tcc gac gac aac ggc Glu Ser Glu Glu Ser Ser Ile Ser Val Asp Glu Ser Asp Asp Asn Gly			1104
355	360	365	
			1152
agt ttt agc cac tac aga tta aac acg cgg tca tct gag acg gca att Ser Phe Ser His Tyr Arg Leu Asn Thr Arg Ser Ser Glu Thr Ala Ile			1152
370	375	380	
			1200
cct gag gaa aac att gat gac ttt gcc agt gcg gaa tta ttt agc aaa Pro Glu Glu Asn Ile Asp Asp Phe Ala Ser Ala Glu Leu Phe Ser Lys			1200
385	390	395	400
			1248
gtc acc gaa caa aat gta agt gac gaa aac tac ata ccg atg aat cca Val Thr Glu Gln Asn Val Ser Asp Glu Asn Tyr Ile Pro Met Asn Pro			1248
405	410	415	
			1296
gtc aat cct acc gat gct atc cat gaa aag gag aag gct gat atg cag Val Asn Pro Thr Asp Ala Ile His Glu Lys Glu Lys Ala Asp Met Gln			1296
420	425	430	
			1344
aga ttg gaa gat gct tcg ctg cat ttc aac ttt ccg gag cac gcg tcg Arg Leu Glu Asp Ala Ser Leu His Phe Asn Phe Pro Glu His Ala Ser			1344

435	440	445	
gaa aag ctt gct aag gat ttt gat ctg gac tct gat aac caa tgc tgt			1392
Glu Lys Leu Ala Lys Asp Phe Asp Leu Asp Ser Asp Asn Gln Cys Cys			
450	455	460	
cgt ccc att cgc gcc tat tcg ata ggc aac aag gtt gag cat tta aag			1440
Arg Pro Ile Arg Ala Tyr Ser Ile Gly Asn Lys Val Glu His Leu Lys			
465	470	475	480
ttt aat aag cgc ctg gga cac ttg aat gat acg gga cag aat ccg aat			1488
Phe Asn Lys Arg Leu Gly His Leu Asn Asp Thr Gly Gln Asn Pro Asn			
485	490	495	
cgc gtg cga gcc tac tcg gtt ggc tcc aaa tcg aag ata ccg cgc tgc			1536
Arg Val Arg Ala Tyr Ser Val Gly Ser Lys Ser Lys Ile Pro Arg Cys			
500	505	510	
gac ctg cag cga gtg gtc ctc gtg gag gac aat aaa cat gag ttc aca			1584
Asp Leu Gln Arg Val Val Leu Val Glu Asp Asn Lys His Glu Phe Thr			
515	520	525	
gcg aat agg agt cag agt agc att acc aag gaa gga acc agc tat ggc			1632
Ala Asn Arg Ser Gln Ser Ser Ile Thr Lys Glu Gly Thr Ser Tyr Gly			
530	535	540	
agc agt gcc aat cga caa aag aag tcc aca agt gct cca ctc ctc agt			1680
Ser Ser Ala Asn Arg Gln Lys Lys Ser Thr Ser Ala Pro Leu Leu Ser			
545	550	555	560
ctg aag aac cag ata aac tcc gac cga atg agt gac tta atg gaa att			1728
Leu Lys Asn Gln Ile Asn Ser Asp Arg Met Ser Asp Leu Met Glu Ile			
565	570	575	
gat ttt tca caa gca acc aat ttg gaa aag cag aag ttc atc aag aat			1776
Asp Phe Ser Gln Ala Thr Asn Leu Glu Lys Gln Lys Phe Ile Lys Asn			
580	585	590	
aat gaa att ccg aaa tac att gaa aac gtg ttc cca aaa gcc ccg cga			1824
Asn Glu Ile Pro Lys Tyr Ile Glu Asn Val Phe Pro Lys Ala Pro Arg			
595	600	605	
acg gat agc tcc agc cta act ctg cac gcc aca agt caa aag gac att			1872
Thr Asp Ser Ser Ser Leu Thr Leu His Ala Thr Ser Gln Lys Asp Ile			
610	615	620	
ttc aat ggc acc aaa cta aat aac act gcg atc aca tcc gag gat ggt			1920
Phe Asn Gly Thr Lys Leu Asn Asn Thr Ala Ile Thr Ser Glu Asp Gly			

625	630	635	640	
tac ctc gag atg aag cca gtc ggt aat gga tac act ccc agt tcg aat				1968
Tyr Leu Glu Met Lys Pro Val Gly Asn Gly Tyr Thr Pro Ser Ser Asn				
645	650	655		
tgc ctg cca atg aaa gtg gag aaa ctc aag cta tcc gac tat cag aca				2016
Cys Leu Pro Met Lys Val Glu Lys Leu Lys Leu Ser Asp Tyr Gln Thr				
660	665	670		
gca ccg cca ctc acc gca aca gcc gca cca gtg cac gat tta aac aaa				2064
Ala Pro Pro Leu Thr Ala Thr Ala Ala Pro Val His Asp Leu Asn Lys				
675	680	685		
att agc aca tac aat ata tcc gct gag aaa tgg aga gaa cag ccc agc				2112
Ile Ser Thr Tyr Asn Ile Ser Ala Glu Lys Trp Arg Glu Gln Pro Ser				
690	695	700		
aga agc gag gaa aag tcg aac tcg cca ttg aat gac aac acc ttt				2160
Arg Ser Glu Glu Lys Lys Ser Asn Ser Pro Leu Asn Asp Asn Thr Phe				
705	710	715	720	
agc tcg aaa ccc aca aat gtc gag agt aca agc aaa agc cat gat gtt				2208
Ser Ser Lys Pro Thr Asn Val Glu Ser Thr Ser Lys Ser His Asp Val				
725	730	735		
cat tca gca aat caa att gat tgc gag aaa gtg tgc gcg cag agc agc				2256
His Ser Ala Asn Gln Ile Asp Cys Glu Lys Val Cys Ala Gln Ser Ser				
740	745	750		
gat aag cta aat aat cat ctg gcc gac aag att gtc gag aac aac aat				2304
Asp Lys Leu Asn Asn His Leu Ala Asp Lys Ile Val Glu Asn Asn Asn				
755	760	765		
ttg gat ata ggc ggg cat gag gaa aag aag ttg gtt cat tcg ata agc				2352
Leu Asp Ile Gly Gly His Glu Glu Lys Lys Leu Val His Ser Ile Ser				
770	775	780		
agc gaa gac tac aca caa atc aag gac aaa tcg aat gat ttc aca aaa				2400
Ser Glu Asp Tyr Thr Gln Ile Lys Asp Lys Ser Asn Asp Phe Thr Lys				
785	790	795	800	
ttt aac gaa gcc ggc tac aaa att ctg caa att aaa agc gac agc tca				2448
Phe Asn Glu Ala Gly Tyr Lys Ile Leu Gln Ile Lys Ser Asp Ser Ser				
805	810	815		
ctc atc tca tcg aag cta tac caa aag ggt ata cac aag gat aac ttg				2496
Leu Ile Ser Ser Lys Leu Tyr Gln Lys Gly Ile His Lys Asp Asn Leu				

820

825

830

gag cgt tcg cag aga ctt aca gag agt gtg aat acg att ccc gat aat 2544
Glu Arg Ser Gln Arg Leu Thr Glu Ser Val Asn Thr Ile Pro Asp Asn
835 840 845

gcc acc gcc acc gcg gtg agc agc tca ctc acc aaa ttc aat ata 2592
Ala Thr Ala Thr Ala Val Ser Ser Ser Leu Thr Lys Phe Asn Ile
850 855 860

aat tca gca aag cca gcc gcc gat tcg cgt agc act ggc aca 2640
Asn Ser Ala Lys Pro Ala Ala Ala Asp Ser Arg Ser Thr Gly Thr
865 870 875 880

gat cca agt aca cca cag aac att cta cag att aaa gat ttg aat ttc 2688
Asp Pro Ser Thr Pro Gln Asn Ile Leu Gln Ile Lys Asp Leu Asn Phe
885 890 895

ccc tca agg tcg tcg tct cgc ata tcc cag ccg gag ctg cac tac gcc 2736
Pro Ser Arg Ser Ser Arg Ile Ser Gln Pro Glu Leu His Tyr Ala
900 905 910

agc cta gat ctt ccc cat tgc agt ggc caa aat cca gct aaa tac ctg 2784
Ser Leu Asp Leu Pro His Cys Ser Gly Gln Asn Pro Ala Lys Tyr Leu
915 920 925

aag aga gga tca cgc gaa tcg ccg ccg gtg tcc gca tgc ccg gag gat 2832
Lys Arg Gly Ser Arg Glu Ser Pro Pro Val Ser Ala Cys Pro Glu Asp
930 935 940

ggg aat acc tat gcg aaa atc gac ttt gac caa tcc gac tcc tct tcc 2880
Gly Asn Thr Tyr Ala Lys Ile Asp Phe Asp Gln Ser Asp Ser Ser Ser
945 950 955 960

tcc tca tcg aac ata ttt aat acg taa 2907
Ser Ser Ser Asn Ile Phe Asn Thr
965

<210> 3

<211> 969

<212> PRT

<213> *Drosophila melanogaster*

<400> 3

Met Ala Ser Ile Ser Asp Asp Gly Met Ala Leu Ser Gly Tyr Leu Lys
1 5 10 15

Lys Leu Lys Thr Met Lys Lys Phe Phe Val Leu Tyr Glu Glu Thr
20 25 30

Ser Thr Ser Ala Ala Arg Leu Glu Tyr Tyr Asp Thr Glu Lys Lys Phe
35 40 45

Leu Gln Arg Ala Glu Pro Lys Arg Val Ile Tyr Leu Lys Asn Cys Phe
50 55 60

Asn Ile Asn Arg Arg Leu Asp Thr Lys His Arg Phe Val Ile Val Leu
65 70 75 80

Ser Ser Arg Asp Gly Gly Phe Gly Ile Val Leu Glu Asn Glu Asn Asp
85 90 95

Leu Arg Lys Trp Leu Asp Lys Leu Leu Val Leu Gln Arg Asn Ile Ala
100 105 110

Asn Ser Asn Gly Thr Ala His Ser Pro Tyr Asp His Val Trp Gln Val
115 120 125

Val Ile Gln Lys Lys Gly Ile Ser Glu Lys Val Gly Ile Thr Gly Thr
130 135 140

Tyr His Cys Cys Leu Thr Ser Lys Ser Leu Thr Phe Val Cys Ile Gly
145 150 155 160

Pro Glu Lys Thr Pro Asn Gly Glu Asp Arg Val Ala Ser Ile Glu Ile
165 170 175

Leu Leu Thr Thr Ile Arg Arg Cys Gly His Ala Ser Pro Gln Cys Ile
180 185 190

Phe Tyr Val Glu Leu Gly Arg Gln Ser Val Leu Gly Ser Gly Asp Leu
195 200 205

Trp Met Glu Thr Asp Asn Ala Ala Ile Ala Thr Asn Met His Asn Thr
210 215 220

Ile Leu Ser Ala Met Ser Ala Lys Thr Glu Ser Asn Thr Asn Leu Ile
225 230 235 240

Asn Val Tyr Gln Asn Arg Pro Asp Leu Ser His Glu Pro Met Arg Lys
245 250 255

Arg Ser Ser Ser Ala Asn Glu Ala Ser Lys Pro Ile Asn Val Asn Val
260 265 270

Ile Gln Asn Ser Gln Asn Ser Leu Glu Leu Arg Ser Cys Ser Ser Pro

275

280

285

His Asn Tyr Gly Phe Gly Arg Glu Arg Cys Asp Ser Leu Pro Thr Arg

290

295

300

Asn Gly Thr Leu Ser Glu Ser Ser Asn Gln Thr Tyr Phe Gly Ser Asn

305

310

315

320

His Gly Leu Arg Ser Asn Thr Ile Ser Gly Ile Arg Pro His Ser Thr

325

330

335

Asn Lys His Ser Asn Ser Pro Thr Phe Thr Met Pro Leu Arg Cys Ser

340

345

350

Glu Ser Glu Glu Ser Ser Ile Ser Val Asp Glu Ser Asp Asp Asn Gly

355

360

365

Ser Phe Ser His Tyr Arg Leu Asn Thr Arg Ser Ser Glu Thr Ala Ile

370

375

380

Pro Glu Glu Asn Ile Asp Asp Phe Ala Ser Ala Glu Leu Phe Ser Lys

385

390

395

400

Val Thr Glu Gln Asn Val Ser Asp Glu Asn Tyr Ile Pro Met Asn Pro

405

410

415

Val Asn Pro Thr Asp Ala Ile His Glu Lys Glu Lys Ala Asp Met Gln

420

425

430

Arg Leu Glu Asp Ala Ser Leu His Phe Asn Phe Pro Glu His Ala Ser

435

440

445

Glu Lys Leu Ala Lys Asp Phe Asp Leu Asp Ser Asp Asn Gln Cys Cys

450

455

460

Arg Pro Ile Arg Ala Tyr Ser Ile Gly Asn Lys Val Glu His Leu Lys

465

470

475

480

Phe Asn Lys Arg Leu Gly His Leu Asn Asp Thr Gly Gln Asn Pro Asn

485

490

495

Arg Val Arg Ala Tyr Ser Val Gly Ser Lys Ser Lys Ile Pro Arg Cys

500

505

510

Asp Leu Gln Arg Val Val Leu Val Glu Asp Asn Lys His Glu Phe Thr

515

520

525

Ala Asn Arg Ser Gln Ser Ser Ile Thr Lys Glu Gly Thr Ser Tyr Gly
530 535 540

Ser Ser Ala Asn Arg Gln Lys Lys Ser Thr Ser Ala Pro Leu Leu Ser
545 550 555 560

Leu Lys Asn Gln Ile Asn Ser Asp Arg Met Ser Asp Leu Met Glu Ile
565 570 575

Asp Phe Ser Gln Ala Thr Asn Leu Glu Lys Gln Lys Phe Ile Lys Asn
580 585 590

Asn Glu Ile Pro Lys Tyr Ile Glu Asn Val Phe Pro Lys Ala Pro Arg
595 600 605

Thr Asp Ser Ser Ser Leu Thr Leu His Ala Thr Ser Gln Lys Asp Ile
610 615 620

Phe Asn Gly Thr Lys Leu Asn Asn Thr Ala Ile Thr Ser Glu Asp Gly
625 630 635 640

Tyr Leu Glu Met Lys Pro Val Gly Asn Gly Tyr Thr Pro Ser Ser Asn
645 650 655

Cys Leu Pro Met Lys Val Glu Lys Leu Lys Leu Ser Asp Tyr Gln Thr
660 665 670

Ala Pro Pro Leu Thr Ala Thr Ala Ala Pro Val His Asp Leu Asn Lys
675 680 685

Ile Ser Thr Tyr Asn Ile Ser Ala Glu Lys Trp Arg Glu Gln Pro Ser
690 695 700

Arg Ser Glu Glu Lys Lys Ser Asn Ser Pro Leu Asn Asp Asn Thr Phe
705 710 715 720

Ser Ser Lys Pro Thr Asn Val Glu Ser Thr Ser Lys Ser His Asp Val
725 730 735

His Ser Ala Asn Gln Ile Asp Cys Glu Lys Val Cys Ala Gln Ser Ser
740 745 750

Asp Lys Leu Asn Asn His Leu Ala Asp Lys Ile Val Glu Asn Asn Asn
755 760 765

Leu Asp Ile Gly Gly His Glu Glu Lys Lys Leu Val His Ser Ile Ser
770 775 780

Ser Glu Asp Tyr Thr Gln Ile Lys Asp Lys Ser Asn Asp Phe Thr Lys
785 790 795 800

Phe Asn Glu Ala Gly Tyr Lys Ile Leu Gln Ile Lys Ser Asp Ser Ser
805 810 815

Leu Ile Ser Ser Lys Leu Tyr Gln Lys Gly Ile His Lys Asp Asn Leu
820 825 830

Glu Arg Ser Gln Arg Leu Thr Glu Ser Val Asn Thr Ile Pro Asp Asn
835 840 845

Ala Thr Ala Thr Ala Val Ser Ser Ser Ser Leu Thr Lys Phe Asn Ile
850 855 860

Asn Ser Ala Lys Pro Ala Ala Ala Asp Ser Arg Ser Thr Gly Thr
865 870 875 880

Asp Pro Ser Thr Pro Gln Asn Ile Leu Gln Ile Lys Asp Leu Asn Phe
885 890 895

Pro Ser Arg Ser Ser Arg Ile Ser Gln Pro Glu Leu His Tyr Ala
900 905 910

Ser Leu Asp Leu Pro His Cys Ser Gly Gln Asn Pro Ala Lys Tyr Leu
915 920 925

Lys Arg Gly Ser Arg Glu Ser Pro Pro Val Ser Ala Cys Pro Glu Asp
930 935 940

Gly Asn Thr Tyr Ala Lys Ile Asp Phe Asp Gln Ser Asp Ser Ser Ser
945 950 955 960

Ser Ser Ser Asn Ile Phe Asn Thr
965

<210> 4

<211> 5210

<212> DNA

<213> *Drosophila melanogaster*<400> 4
agaacgactt tttcctcctt agtcagtcac aagaaaaacta aagcttacca acaatacggc 60

gtgtattgtt aaatttattac aacaaataaa atattcaaat tgtatTTaaa aatatagtaa 120

ccattaaaaa ataaaatcaa tatgcgaaac tttgtaattt cttaactcatc cttgttttt 180

tggaaatcat ggcataata tcggatgacg gcatggcgct gagtggctac ctcaagaagc 1680
tgaagaccat gaagaagaag ttctttgtgc tgtacgagga gacgagcact tcggcagccc 1740
ggctggagta ctacgatacc gaaaagaagt tcctgcaaag agccgagcca aaaagggtta 1800
tctatctgaa gaattgcttc aacatcaatc gccgtttgga caccaagcat agatttgc 1860
tttgctctc ctccagagac ggtggattcg gcatcggtct cgagaacgaa aatgatttac 1920
gcaaatggtt ggacaaacta ctagttctac aaaggaacat agccaattcg aatggaacag 1980
cgcaactcacc ttatggatg ccaaataaac tataactacc agtttagtatg aaacctaaac 2040
acttcatttc actttgcaga ccacgttgg caagttgtca ttcaaaagaa gggtatttcg 2100
gagaaagttg gaatcaccgg aacctaccac tggcctta cttcaaaatc cctgacattc 2160
gtgtgcattg gacccggagaa gacgcccattt ggcgaggatc gcgttgcgag cattgaaata 2220
cttttgcacca cgatcaggcg gttagttgtt gccagcaaaa ctgcaaggaa ttgtaaaata 2280
attcggactt aatttcagat gcggtcatgc atccccacaa tgtatattct acgtggaact 2340
tggccgccaa agtgtcttgg gatctggta tctgtggatg gagacggata acgcagctat 2400
tgctactaat atgcacaaca cgataactgag gtattnatct ctcattacaa ctaatccaag 2460
atttcatgat catcctacaa aacgacatag atagtttaag atatctccca gttaacttta 2520
ataattctgt gggtttttc tttcagcgct atgtcagccaa acacagatc gaacacgaaat 2580
ttaataaacg tttatcagaa cagacctgac ttaagtcacg agcccatgag aaagcgatcg 2640
tcgtctgcaa acgaaggatc gaagccgata aacgtaaatg tcataacaaa tagtcaaaac 2700
tctctcgaat tgcgcagctg cagttcgccc cataactatg gtaataactt caaatgtatg 2760
tttaaacgca aaattaatca aacgcaatcg tttcaggttt cggcagagag agatgcgata 2820
gcttaccaac cagaaatgga accctaagcg agtccagccaa tcaaacgtac tttggttcca 2880
accatggact gcgatccaaat actatatctg gcatccgtcc gcactcaacc aacaagcata 2940
gtaatagtcc aacgttcacc atgccattaa gatgctcaga atccgaagag tcatcaatta 3000
gtgtcgatga atccgacgac aacggcagtt ttagccacta cagattaaag tgcgttgcta 3060

tcaaataata attatttaat aataatcacc atttcaattt ctagcacgct gtcatctgag 3120
acggcaattc ctgaggaaaa cattgatgac tttgccagtg cggaatttatt tagcaaagtc 3180
accgaacaaa atggtaagcc aaacacaaaa acaattttt aacatgaaaa gtagctaattc 3240
aattggcttt gttaactgc agtaagtgc gaaaactaca taccgatgaa tccagtcatt 3300
cctaccgatg ctatccatga aaaggagaag gctgatgc agagattgga agatgcttcg 3360
ctgcatttca acttccgga gcacgcgtcg gaaaagcttgc ttaaggattt tgatctggac 3420
tctgataacc agtgagtaca catttcgctt caactgtgcc acgtaatgca atcaatcaca 3480
tcttgttaca gatgctgtcg tcccattcgc gcctattcga taggcaacaa ggttgagcat 3540
ttaaagttta ataagegcct gggacacttg aatgatacgg gacagaatcc gaatcgctg 3600
cgaggctact cggttggctc caaatcgaag ataccgcgtc gcgacctgca gcgagtggtc 3660
ctcgtggagg acaataaaca tgagttcaca gogaatagga gtcagagtag cattaccaag 3720
gaaggaacca gctatggcag cagtgcctt cgcacaaaaga agtccacaaag tgctccactc 3780
ctcagtctga agaaccagat aaactccgac cgaatgagtg acttaatgga aattgatttt 3840
tcacaagcaa ccaatttggaa aaagcagaag ttcataaga ataatgaaat tccgaaatac 3900
attgaaaacg tgccccaaa agccccgcga acggatagct ccagcctaac tctgcacgccc 3960
acaagtcaaa aggacatttt caatggcacc aaactaaata acactgcgt cacatccgag 4020
gatggttacc tcgagatgaa gccagtcggt aatggataca ctcccagttc gaattgcctg 4080
ccaatgaaag tggagaggct caagctatcc gactatcaga cagcaccgc aatcaccgca 4140
acagccgcac cagtgcacga tttaaacaata attagcacat acaatatac cgctgagaaa 4200
tggagagaac agcccagcag aagcgagggaa aagaagtcga actcgccatt gaatgacaac 4260
acctttggct tgaaacccac aaatgtcgag agtacaagca aaagccatga tgttcattca 4320
gcaaatcaaa ttgattccga gaaagtgtgc ggcagagca ggcataagct aaataatctg 4380
gccgacaaga ttgtcgagaa caacaatttg gatataaggcg ggcattgagga aaagaagttg 4440
gttcattcga taagcagcga agactacaca caaatcaagg acaaatcgaa tgatttcaca 4500

aaatttaacg aagccggcta caaaattctg caaattaaaa ggcgacagctc actcatctca 4560
tcgaagctat accaaaaggg tatacacaag gataacttgg agcggtcgca gagacttacg 4620
gagagtgtga atacgattcc cgataatgcc accgccaccc cggtgagcag cagctcactc 4680
accaaattca atataaattc agcaaagcca gcccggccg ccgattcgcg tagcactggc 4740
acagatccaa gtacaccaca gaacattcta cagattaaag atttgaattt cccctcaagg 4800
tcgtcgctc gcatatccca gccggagctg cactacgcca gcctagatct tccccattgc 4860
agtggccaaa atccagctaa atacctgaag agaggatcac gcgaatcgcc gccgggtgtcc 4920
gcatgccccg aggatggaa tacctatgcg aaaatcgact ttgaccaatc cgactcctct 4980
tcctcctcat cgaacatatt taatacgtaa agtttgaaa tttatgaccc tattctatata 5040
atatgatttg tttaatattt tacatttattt gtaaatattt tctgacaagg aaagcttaca 5100
attttggatg ctaataaata aattttattt aaattataat gatccctttg gactttttt 5160
tttttggac taagaaatca ctactaaaga agggctttc gagggttaaa 5210